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Minimum DB :
Maximum DB :
                                                                                                                                                                                                                                                                                                                          Result
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Maximum Match 10
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Perfect score:
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                                                                                                                                                                                                                                                                                                       Score
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length: 2000000000
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhe:*
8: sp_organel1:
9: sp_phage:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
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sp_mammal:*
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Q9VSY5
Q9YU52
Q9W153
Q9W1J3
Q9S1U6
Q9W1J3
Q8S5U8
Q9W1J3
Q8S5U8
Q9W1J3
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196.351 Million cell
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                                                                 O96se4 homo sapien
O9neb6 Leishmania
O9neb6 Leishmania
O911c6 white spot
O49289 arabidopsis
O9vsv5 drosophila
O9tv97 drosophila
O9tv97 drosophila
O8ru52 oryza sativ
O94e54 oryza sativ
O9wn13 drosophila
                Q8s5u8 oryza sativ
O50357 lactobacill
Q8r1s6 mus musculu
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4 15.3	15.3 455 5	4 15.3 330 5 Q	15.3 131 17	15.3 113 5 Q	15.4 3436	15.4 840 5 Q	15.4 527 4	15.4 461 4 Q	15.4 178 10	15.4 129 10	15.6 726 10	15.6 595 10	15.6 389 3	15.6 385 5	15.6 333 3 Q	15.6 80 10	15.7 1783 5 Q	65.5 15.7 553 11 Q8VE08	15.7 113 10	15.8 3025 5 Q	15.9 458 16	15.9 151	16.0 1145 3	16.0 853 5	16.0 808 5	16.0 386 5 Q	16.0 329 10	7 16.0
P79994 gallus gall	Q960c1 drosophila	Q23073 caenorhabdi	0		Q66666 equine herp	Q95yf6 patinopecte	095747 homo sapien	Q9upq1 homo sapien		Q02090 lycopersico	Q9awx4 oryza sativ	Q8s826 oryza sativ	Q96u39 neurospora	Q9vft2 drosophila	Q9hfl2 neurospora	Q9suf7 arabidopsis	Q9vx48 drosophila		œ		σ	Q96lu0 homo sapien	094043 candida alb		Q9v995 drosophila	Q24486 drosophila	Q91gv0 oryza sativ	001844 caenorhabdi

## ALIGNMENTS

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RESULT 2
Q96SE4
ID Q96S
AC Q96S
Q96SE4;
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Q8SSX0;
Q1-UUN-2002 (TrEMBLrel. 21, Created)
Q1-UUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Protein localized in the NUCLEOLI. 6/101.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Gulgo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and Analysis of Chromosome 2 of Dictyostelium."; "Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC115580; AAL92217.1; -

EMBL; AC11580; AAL92217.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AX4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                           204 FAFVSFDSEDAVEKA-IALTGTKFEGREIQVERSQRGGGRSSSFGRGGGRGGFGGGRGGR
                                                                                                                                                                                                                                  70 GGTADTGG
                                                                                                                                                                                                                                                                                                                                                  10 YLFIYFLSYSLGDRARLCLRKTKQQQKEQQILRQSEVLFRSETLRKTGKKGRRWGGQGGR 69
                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                 PRELIMINARY;
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                                    2724
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Best Local S
Matches 24
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01-OCT-2000
01-OCT-2000
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01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00270; DEAD; 1.
Pfam; PF00476; DNA_POl_A; 1.
Pfam; PF00271; helicase_C; 1.
PROSITE; PS00447; DNA_POLXMERASE_A; UNKNOWN_1.
ATP-binding; Helicase.
SEQUENCE 2724 AA; 305148 MW; 30B88663614E6;
                                        Genome Res. 8:135-145(1998).
EMBL; AL157415; CAB75639.1; -.
HSSP; P17119; 3KAR.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                         Bothe G.,
Barrell B.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR_DOMAIN2; 1.

ATP-binding; Coiled coil; Microtubules; Motor protein.

SEQUENCE 1254 AA; 132206 MW; 79350B2FBC82B2D0A CRC64;
                                                                                                                                                                                                                                                                           L8325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abbas A.R., Linn S.M.;
"Homo sapiens polymerase (DN Submitted (APR-2001) to the EMBL; AY032677; AAK39635.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
Mammalia; F
                                                                                                     "A physical map of the Leishmania
                                                                                                                 Ivens A.C.,
Smith D.F.;
                                                                                                                                    MEDLINE-98146435;
                                                                                                                                                  STRAIN-FRIEDLIN;
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                               Submitted
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                                                                                                                                                                                                                                           Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                     Kinesin-like
                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                         Q9NEB6
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InterPro; IPR001098; DNA_pol.
InterPro; IPR001650; Helicase_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             LGDRARLC-LRKTKQQQKEQQILRQSEVLFRSET-----
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; Metazoa; Chordata;
Eutheria; Primates;
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                                                                                                                                      PubMed=9477341;
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19,
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                                                                                                                                                                                                 A.C., Quail M.,
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Last sequence
Last anno
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Last
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                               sequence up
annotation
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annotation
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                                                                                                      Friedlin
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                                                                                                     genome
                                                                                                                          Chan H.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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RESIDENT RESIDENT RESIDENT RESIDENT REPORTED TO THE REPORT REPORT
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01-DEC-2001
01-DEC-2001
                                     Yang F., E
Submitted
                                                       SEQUENCE Yang F.,
                                                                                                                                                                                                                                                                  White spot syndrome viviruses; unclassified
                                                                                                                                                                                                                                                                                                                       Q8VAY1;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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MEDLINE=21342572; PubMed=11448154;
Tanchini R., Fiers M., Sandbrink H.,
Tarchini R., Fiers M., Sandbrink H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           verily, gene family 8.
White spot syndrome virus (WSSV).
Viruses; unclassified virus
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                                                                                                                                                                                                                                                                                                         WSv238 (WSSV294).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van Hulten M.C.W., Witteveldt J., Peters S., F
Tarchini R., Fiers M., Sandbrink H., Lankhorst
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AF369029; AAK77788 1;
                                                                                                                                  virus
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-21548311; PubMed-11689662;
                                                                                                                                                                                                                                                                                                                                                                                                      Q8VAY1
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21,
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Last sequence
Last annotation
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Pred. No. 2.3;
19; Mismatches
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Pred. No. 4.9;
10; Mismatches
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he shrimp
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annotation
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H., Lankhorst R.K., Vlak J.
A genome sequence.";
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O49289;
O1-JUN-1998 (TrEMBLrel. 06
01-JUN-1998 (TrEMBLrel. 06
01-DEC-2001 (TrEMBLrel. 19
F22K20.13 protein.
                                                                                                                      STRAIN-CV. COLUMBIA; rederspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Cor rederspiel N.A., Buehler E., Dewar K., Feng J., Kim C., Oli O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysc Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                               InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helica
Pfam; PR00270; DEAD; 1.
Pfam; PR00271; helicase_C;
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EMBL; AF332093; AAL33242.1; -
EMBL; AF440570; AAL89162.1; -
SEQUENCE 486 AA; 51463 MW;
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"Identification and characterization of a shrimp white spot virus (WSSV) gene that encodes a novel chimeric polypeptide cellular-type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
                                                                                                   EMBL; AC00229;
HSSP; Q58083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a nucleocapsid protein (VP35) gene of shrimp spot syndrome virus and characterization of the motif important targeting VP35 to the nuclei of transfected insect cells."; Virology 293:44-53(2002).
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Lo C.F., F
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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LO C.-F., KOU
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MEDLINE-21844071;
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                                                                                                                  AC002291; AAC00620.1;
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                       SM00487; DEXDc; 1.
SM00490; HELICC; 1.
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H., Huang C.J., Chou
  93503 MW;
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27.0%;
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  3CA33435AC400497 CRC64;
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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,

RA Ballew R.M., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Butler H., Caddeu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Breits S.M.,

RA Dodson K., Dopt L.E., Domes M., Dugan-Rocha S., Dunkov B.C.,

RA Glodek R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Weil M.-H., Ibeyaan C.,

RA Harris N.L., Harvey D., Helman T.J., Weil M.-H., Ibeyaan C.,

RA Harris N.L., Harvey D., Helman T.J., Weil M.-H., Ibeyaan C.,

RA Liu X., Mattel B., McIntosh T.C., Mratic M.H., McBeac M.G.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Ketchum K.A.,

RA Harris M., Malsoh F., Karpen G.H., Ke Z., Kennington D.,

RA McIntosh M., Malsoh R.A., Mis
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                              FlyBase; FBgn0028431; Glu-RIB
InterPro; IPR001828; ANF_rece
EnterPro; IPR001320; Ion_glu_
InterPro; IPR001622; K+channe
InterPro; IPR001311; SBP/glu_
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NCBI_TaxID=7227;
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Mismatches
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RESULT OF THE PROPERTY OF THE 
1 OSTWG7;
2 OSTWG7;
3 OSTWG7;
4 O1-MAY-2000 (TREMBLIEL 13, Created)
4 O1-MAY-2000 (TREMBLIEL 13, Last sequence update)
5 O1-MAY-2000 (TREMBLIEL 13, Last sequence update)
6 O1-MAY-2000 (TREMBLIEL 13, Last annotation update)
7 O1-JUN-2002 (TREMBLIEL 12, Last annotation update)
7 O1-JUN-2002 (TREMBLIEL 13, Last annotation update)
7 O1-JUN-2002 (TREMBLIEL 13, Last annotation update)
7 O1-JUN-2002 (TREMBLIEL 13, Created)
7 O1-JUN-2002 (TREMBLIEL 13, C
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ProDom; PD000500; I
SMART; SM00079; PBP
SEQUENCE 1049 AA;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                Q8RU52 PRELIMINARY; PRT; 1150 AA. Q8RU52; Q1-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative copia-like retrotransposon hopscotch polosynbb0048022.20.
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InterPro; IPR001622; K+channel_pore.
InterPro; IPR001311; SBP/glu_receptor.
Pfam; PF00060; 11g_chan; 1.
PRINTS; PR01582; KV33CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WT BERLIN, AND CANTON S;
Voelkner M., Lenz-Boehme B., Fuchs S., Wismar J., Betz H., Schmitt Poelkner M., Lenz-Boehme B., Fuchs S., Wismar J., Betz H., Schmitt Poels of Drosophila melanogaster.
"Novel glutamate receptor subunit genes of Drosophila melanogaster. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ251887; CAB64940.1; -.
EMBL; AJ251886; CAB64939.1; -.
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FlyBase; FBgn0028431; Glu-RIB.
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s; PR01582; KV33CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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1095 AA;
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1049 AA; :
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· 120782 »
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32.7%;
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Pred. No. 11;
6; Mismatches
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Pred. No. 11;
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                                                                                                                                                               notation update)
hopscotch polyprotein
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a; Brachycera;
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Q9SNU6 ID QS AC QS DT 01

Q9SNU6; Q9SNU6; 01-MAY-2000 01-MAY-2000

(TrEMBLrel. (TrEMBLrel.

13, 13,

Created) Last sequ

sequence

update)

PRELIMINARY;

PRT;

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Q94E54
ID Q94E5
ID Q94E5
AC Q94E5
AC Q94E5
DT Q1-DE
DT Q1-DE
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DE ENKAR
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Best Local
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EMBL; AP003215; BAB62558.1; -.
InterPro; IPR004827; TF_bZIP.
Pfam; PF00170; bZIP; 1.
PROSITE; PS00036; BZIP_BASIC; U
SEQUENCE 203 AA; 21092 MW;
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STRAIN-(V. NIPPONBARE;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.
Oryza sativa chromosome 10 BAC OSJNBb0048022 genomic sequence.*;
Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamar
"Oryza sativa nipponbare(GA3)
clone:OSJNBa0089K24.";
                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae;
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01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative THY5 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AC099325; AAM18766.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
 11
                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                Local
                                                                                             105
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                                                                                                                                                                Similarity
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                                                                                                                       SLGDRARLCLRK-----TKQQQKEQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGRGRGGGNRGRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGGQGGRGGTADTGG
                                        TLRQILKNTTAHAGKRGGGGGGKGGDGGGGG
                                                                                             SAGDKEQNRLKRLLRNRVSAQQARERKKAYMTELEAKAKDLELRNAELEQRVSTLQNENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSYLLSSLAREILTQVVSIETAAELWRTLENMLCSQTENYHKMNSFSDEMAMTTTRKGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSYSLGDRARLCLRKTKQQQKEQQILRQSEVL-----
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                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                   -TGKKGRRWGGQGGRGGTADTGG
                                                                                                                                                               16.5%;
26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.6%;
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19,
21,
                                                                                                                                                                                                                                                                                                             Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                          Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.5; D
Pred. No. 15;
7; Mismatches
                                                                                                                                                                Score 69; I
Pred. No. 2.
                                                                                                                                                                                                      UNKNOWN_1.
C796B3659CD9255F CRC64;
                                                                                                                                                                                                                                                                                               genomic
                                                                                                                                                                                                                                                                                                                                                                                            Liliopsida;
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48533604BFF3D620 CRC64;
                                                                                                                                                                                                                                                                                               DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                            DB
7.6;
                                          195
                                                                   77
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                                                                                                                                                                                                                                                                                                                                                                                              Poales;
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                                                                                                                                                                                                                                                                                                 chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                  22;
                                                                                                                                                                                                                                                                         databases
                                                                                                                                                                            Length 203
                                                                                                                       -ILRQSEVLFRSETLRK----
                                                                                                                                                                                                                                                                                                                                                                                               Poaceae;
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RX MEDLINE-20196006; PubMed-10731132;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Dodson K.T., Deup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Korrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegvam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Wei M.-H., Ibegvam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentson D.R., Pacleb J.M.,
RA Neison D.R., Pacleb J.M.,
RA Reinert K., Reandigton K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos T., Simpson M., Skupski M.P. Smith T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B 8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W1J3;
Q9W1J3;
01-MAY-2000
01-MAY-2000
01-JUN-2002
CG5543 prote
CG5543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; I
Pterygota; Neoptera;
Ephydroidea; Drosoph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG5543 Procession (Fruit fly).
Drosophila melanogaster (Fruit fly).
Drosophila melazoa; Arthropoda; Tracheata; He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone:P0538C01.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AP000391; BAA83351.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel.
ESTs AU077435(C12539).
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NY-2000 (TrEMBLrel. 13, 1)
NY-2002 (TrEMBLrel. 21, 1)
3 protein (LD31556P).
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTSFSTG----QPCISTSPKQEATELGKKARELKKAAEALHQEE---KSGKKGRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLSYSIGDRARICLRKTKQQQ-----KEQQILRQSEVLFRSETLRKTGKKGRRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophilidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.5%;
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 Simpson
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexapoda; Insecta;
a; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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Under C., Chavez C., Dorsett V., Farfan D., Frise E., George R., wonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., RA Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).

EMBL; AB003462; AAAL13853.1; --
DR EMBL; AP058624; AAAL13853.1; --
DR FlyBase; FBgn0034908; CG5543.

DR FlyBase; FBgn0034908; CG5543.

PR PINTS; PR001680; WD40; 7.

PR PRINTS; PR00320; ~~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q8S5U8
                                                                        SO DRIFT AND COCO SOLUTION OF THE SOLUTION OF 
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Query Match
Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002
01-JUN-2002
                                                                SEQUENCE FROM N.A.

Wing R.A., Yu Y., Soderlund C., Chen M., Kim H
Saski C., Henry D., Oates R., Simmons J.;

"Rice Genomic Sequence.";

submitted (APR-2002) to the EMBL/GenBank/DDBJ
EMBL; AC104428; AAM15780.1; -

BMBL; AC104428; AAM15780.1; -

SEQUENCE 884 AA; 94539 MW; 1F29B5DBAD0035F
                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group). 
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8S5U8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; V
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                           OJ1123F12
                                                                                                                                                                                                                                                                                                                                                                                                                               Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002
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PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                    NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8S5U8
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 homeodomain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITSGQGGR--VASSGGTLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARLCLRKTKQQQKEQQILRQSEV-----LFRSE---TLRKTGKKGRR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKLCVVKTHRKRQPMEMVGVSQIITPHALPLFRQEKSRTSRKRMEKARMDPVKSQRPDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spradling A.C., Stapleton M., Stron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat.
655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73607 MW; 4A3EF0602E253FEC CRC64;
16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Score 68.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69; 1
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                   Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                protein.
1F29B5DBAD0035F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         884
                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
  5;
                                                                                                                                                                                                              Kim H.-R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                        DB 10;
                                                                                                                                                                                                                                                                                                                                   Poales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 655;
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                                                                        CRC64;
                      Length
                                                                                                                                                                                                                                                                                                                                     Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                Rambo
                        884;
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Matches

Conservative

Mismatches

14;

Indels

25;

Gaps

4

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RESULT
O50357
ID O50357
AC O50
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ID QRAIS
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AC QRAIS
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DT 01-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 15
                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ003194;
NON_TER 1
SEQUENCE 165 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    050357
050357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 48.0 kDa protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC024127; AAH24127.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8R1S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8R1S6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CcpA & tnp genes (Fragment).
Lactobacillus casei.
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 393;
MEDLINE-98012962; PubMed-9352913;
Monedero V., Gosalbes M.J., Perez-Martinez G.;
"Catabolite repression in Lactobacillus casei ATCC393 is mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 179:6657-6664(1997).
3L; AJ003194; CAA05974.1; -.
     43 QSEVLFRSETLRKTGKKGRRWGGQGGRGGTADTGG 77
                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
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                                                                                                        3 LSTHLFIYLFIYFLSYSLGDRARL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
15; Conserv
                                                                                                                                                                                        Similarity
                                                    ISEHCFDLIFAFDEIVALGYRENVNLAQIRTFTEMDSHEEKVFRAVRETQEREAKAEMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQNQQGTSENPAKVKPQTTGTGGSNGDRTGGTGGTGTTTETG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHWSGGGDGRG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GGQGGRG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHVILSLFFLPLFPFSLSTSA-FCKRRWRQRQR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFIYLFIYFL---SYSLGDRARLCLRKTKQQQKEQQILRQSEVLFRSETLRKTGKKGRRW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AA; 16851 MW;
                                                                                                                                                                                                                                                                     429 AA; 47964 MW;
                                                                                                                                                            16.3%; Scilarity 21.1%; Pr
Conservative 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.3%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6,
                                                                                                                                                                                        Score 68; DB 11; Length 429; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 2; Length 165; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                     40ABE6564EB1BBEA CRC64;
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                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C54BDCC033EE93AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                        ---CLRKTKQQQKEQQILR 42
                                                                                                                                                            22;
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